

=====

Sequence Listing was accepted with existing errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: Fri May 25 11:38:56 EDT 2007

=====

Application No: 10511719 Version No: 2.0

Input Set:

Output Set:

Started: 2007-05-18 10:55:18.304
Finished: 2007-05-18 10:55:19.121
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 817 ms
Total Warnings: 7
Total Errors: 2
No. of SeqIDs Defined: 12
Actual SeqID Count: 12

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 249	Order Sequence Error <213> -> <213>; Expected Mandatory Tag: <400> in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 250	Structural Validation Error; Sequence listing may not be indexable

SEQUENCE LISTING

<110> REGEN Biotech. Inc.

<120> The method for measuring the amount of BetaIG-H3 protein and diagnostic kit using the same

<130> 2fpo-10-14

<160> 12

<170> KopatentIn 1.71

<210> 1

<211> 683

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Leu Phe Val Arg Leu Leu Ala Leu Ala Leu Ala Leu Ala Leu
1 5 10 15

Gly Pro Ala Ala Thr Leu Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu
20 25 30

Val Leu Gln His Ser Arg Leu Arg Gly Arg Gln His Gly Pro Asn Val
35 40 45

Cys Ala Val Gln Lys Val Ile Gly Thr Asn Arg Lys Tyr Phe Thr Asn
50 55 60

Cys Lys Gln Trp Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile
65 70 75 80

Ser Tyr Glu Cys Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly
85 90 95

Cys Pro Ala Ala Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val
100 105 110

Val Gly Ser Thr Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu
115 120 125

Arg Pro Glu Met Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser
130 135 140

Asn Glu Ala Trp Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val
145 150 155 160

Ser Asn Val Asn Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val
165 170 175

Gly Arg Arg Val Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr
180 185 190

Ser Met Tyr Gln Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly
195 200 205

Ile Val Thr Val Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala			
210	215	220	
Thr Asn Gly Val Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr			
225	230	235	240
Asn Asn Ile Gln Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu			
	245	250	255
Arg Ala Ala Val Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn			
	260	265	270
Gly Gln Tyr Thr Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile			
	275	280	285
Pro Ser Glu Thr Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg			
	290	295	300
Asp Leu Leu Asn Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala			
305	310	315	320
Ile Val Ala Gly Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu			
	325	330	335
Val Gly Cys Ser Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile			
	340	345	350
Ser Asn Lys Asp Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp			
	355	360	365
Glu Leu Leu Ile Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala			
	370	375	380
Glu Ser Asp Val Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu			
385	390	395	400
Gly Asn His Leu Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu			
	405	410	415
Asn Ser Val Phe Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg			
	420	425	430
Asn Leu Leu Arg Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr			
	435	440	445
Leu Tyr His Gly Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg			
	450	455	460
Val Phe Val Tyr Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala			
465	470	475	480
Ala His Asp Lys Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg			
	485	490	495
Val Leu Thr Pro Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp			
	500	505	510

Asn Arg Phe Ser Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr
515 520 525

Glu Thr Leu Asn Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn
530 535 540

Glu Ala Phe Arg Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly
545 550 555 560

Asp Ala Lys Glu Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu
565 570 575

Ile Leu Val Ser Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu
580 585 590

Gln Gly Asp Lys Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val
595 600 605

Asn Lys Glu Pro Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val
610 615 620

Val His Val Ile Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln
625 630 635 640

Glu Arg Gly Asp Glu Leu Ala Asp Ser Ala Leu Glu Ile Phe Lys Gln
645 650 655

Ala Ser Ala Phe Ser Arg Ala Ser Gln Arg Ser Val Arg Leu Ala Pro
660 665 670

Val Tyr Gln Lys Leu Leu Glu Arg Met Lys His
675 680

<210> 2
<211> 2691
<212> DNA
<213> Homo sapiens

<400> 2
gcttgccccgt cggtcgctag ctcgctcggt gcgcgctgct ccgctccatg gcgctcttcg 60
tgcggtctgct ggctctcgcc ctggctctgg ccctggggccc cgccgcgacc ctggcgggtc 120
ccgccaagtc gccctaccag ctggtgctgc agcacagcag gctccggggc cgccagcacg 180
gccccaacgt gtgtgctgtg cagaagggtta ttggcactaa taggaagtac ttcaccaact 240
gcaagcagtg gtaccaaagg aaaatctgtg gcaaataaac agtcatcagc tacgagtgtc 300
gtcttgata tgaaaaggtc cctggggaga agggctgtcc agcagcccta ccactctcaa 360
acctttacga gaccctggga gtcgttgat ccaccaccac tcagctgtac acggaccgca 420
cggagaagct gaggcctgag atggaggggc ccggcagctt caccatcttc gccctagca 480
acgaggcctg ggctccttg ccagctgaag tgctggactc cctggtcagc aatgtcaaca 540

ttgagctgct caatgccctc cgctaccata tgggtgggcag gcgagtcctg actgatgagc	600
tgaaacacgg catgaccctc acctctatgt accagaattc caacatccag atccaccact	660
atcctaattgg gattgtaact gtgaactgtg cccggctcct gaaagccgac caccatgcaa	720
ccaacgggggt ggtgcacctc atcgataagg tcatctccac catcaccaac aacatccagc	780
agatcattga gatcgaggac acctttgaga cccttcgggc tgctgtggct gcatcagggc	840
tcaacacgat gcttgaaggc aacggccagt acacgctttt ggccccgacc aatgaggcct	900
tcgagaagat ccctagttag actttgaacc gtatcctggg cgaccagaa gccctgagag	960
acctgctgaa caaccacatc ttgaagtcag ctatgtgtgc tgaagccatc gttgcggggc	1020
tgtctgtaga gaccctggag ggcacgacac tggaggtggg ctgcagcggg gacatgctca	1080
ctatcaacgg gaaggcgatc atctccaata aagacatcct agccaccaac ggggtgatcc	1140
actacattga tgagctactc atcccagact cagccaagac actatttgaa ttggctgcag	1200
agtctgatgt gtccacagcc attgaccttt tcagacaagc cggcctcggc aatcatctct	1260
ctggaagtga gcggttgacc ctctggctc cctgaattc tgtattcaaa gatggaaccc	1320
ctccaattga tgccataca aggaatttgc ttcggaacca cataattaaa gaccagctgg	1380
cctctaagta tctgtaccat ggacagaccc tggaaactct gggcggcaaa aaactgagag	1440
tttttgttta tcgtaatagc ctctgcattg agaacagctg catcgcggcc cacgacaaga	1500
ggggggaggta cgggaccctg ttcacgatgg accgggtgct gacccccca atggggactg	1560
tcatggatgt cctgaaggga gacaatcgct ttagcatgct ggtagctgcc atccagtctg	1620
caggactgac ggagaccctc aaccgggaag gagtctacac agtctttgct ccacaaaatg	1680
aagccttccg agccttgcca ccaagagaac ggagcagact cttgggagat gccaaggaac	1740
ttgccaacat cctgaaatac cacattggtg atgaaatcct ggtagcgga ggcacgggg	1800
ccctggtgcg gctaaagtct ctccaaggtg acaagctgga agtcagcttg aaaaacaatg	1860
tgggtgagtgt caacaaggag cctgttgccg agcctgacat catggccaca aatggcgtgg	1920
tccatgtcat caccaatgtt ctgcagctc cagccaacag acctcaggaa agaggggatg	1980
aacttgca ga ctctgcgctt gagatcttca aacaagcatc agcgttttcc agggcttccc	2040
agaggtctgt gcgactagcc cctgtctatc aaaagttatt agagaggatg aagcattagc	2100
ttgaagcact acaggaggaa tgcaccacgg cagctctccg ccaatttctc tcagatttcc	2160
acagagactg tttgaatgtt ttcaaaacca agtatcacac tttaatgtac atgggccgca	2220

ccataatgag atgtgagcct tgtgcatgtg ggggaggagg gagagagatg tactttttaaa 2280

atcatgttcc ccctaaacat ggctgttaac ccactgcatg cagaaacttg gatgtcactg 2340

cctgacattc acttccagag aggacctatc ccaaagtgtg aattgactgc ctatgccaag 2400

tccttgaaaa aggagcttca gtattgtggg gtcataaaaa catgaatcaa gcaatccagc 2460

ctcatgggaa gtcttggcac agtttttgta aagcccttgc acagctggag aaatggcatc 2520

attataagct atgagttgaa atgttctgtc aaatgtgtct cacatctaca cgtggcttgg 2580

aggcttttat ggggccctgt ccaggtagaa aagaaatggt atgtagagct tagatttccc 2640

tattgtgaca gagccatggt gtgtttgtaa taataaaacc aaagaaacat a 2691

<210> 3

<211> 585

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(585)

<223> 69 to 653 amino acid sequence of human ID No.1

<400> 3

Tyr Gln Arg Lys Ile Cys Gly Lys Ser Thr Val Ile Ser Tyr Glu Cys

1 5 10 15

Cys Pro Gly Tyr Glu Lys Val Pro Gly Glu Lys Gly Cys Pro Ala Ala

20 25 30

Leu Pro Leu Ser Asn Leu Tyr Glu Thr Leu Gly Val Val Gly Ser Thr

35 40 45

Thr Thr Gln Leu Tyr Thr Asp Arg Thr Glu Lys Leu Arg Pro Glu Met

50 55 60

Glu Gly Pro Gly Ser Phe Thr Ile Phe Ala Pro Ser Asn Glu Ala Trp

65 70 75 80

Ala Ser Leu Pro Ala Glu Val Leu Asp Ser Leu Val Ser Asn Val Asn

85 90 95

Ile Glu Leu Leu Asn Ala Leu Arg Tyr His Met Val Gly Arg Arg Val

100 105 110

Leu Thr Asp Glu Leu Lys His Gly Met Thr Leu Thr Ser Met Tyr Gln

115 120 125

Asn Ser Asn Ile Gln Ile His His Tyr Pro Asn Gly Ile Val Thr Val

130 135 140

Asn Cys Ala Arg Leu Leu Lys Ala Asp His His Ala Thr Asn Gly Val

145		150		155		160
Val His Leu Ile Asp Lys Val Ile Ser Thr Ile Thr Asn Asn Ile Gln						
	165		170		175	
Gln Ile Ile Glu Ile Glu Asp Thr Phe Glu Thr Leu Arg Ala Ala Val						
	180		185		190	
Ala Ala Ser Gly Leu Asn Thr Met Leu Glu Gly Asn Gly Gln Tyr Thr						
	195		200		205	
Leu Leu Ala Pro Thr Asn Glu Ala Phe Glu Lys Ile Pro Ser Glu Thr						
	210		215		220	
Leu Asn Arg Ile Leu Gly Asp Pro Glu Ala Leu Arg Asp Leu Leu Asn						
225		230		235		240
Asn His Ile Leu Lys Ser Ala Met Cys Ala Glu Ala Ile Val Ala Gly						
	245		250		255	
Leu Ser Val Glu Thr Leu Glu Gly Thr Thr Leu Glu Val Gly Cys Ser						
	260		265		270	
Gly Asp Met Leu Thr Ile Asn Gly Lys Ala Ile Ile Ser Asn Lys Asp						
	275		280		285	
Ile Leu Ala Thr Asn Gly Val Ile His Tyr Ile Asp Glu Leu Leu Ile						
	290		295		300	
Pro Asp Ser Ala Lys Thr Leu Phe Glu Leu Ala Ala Glu Ser Asp Val						
305		310		315		320
Ser Thr Ala Ile Asp Leu Phe Arg Gln Ala Gly Leu Gly Asn His Leu						
	325		330		335	
Ser Gly Ser Glu Arg Leu Thr Leu Leu Ala Pro Leu Asn Ser Val Phe						
	340		345		350	
Lys Asp Gly Thr Pro Pro Ile Asp Ala His Thr Arg Asn Leu Leu Arg						
	355		360		365	
Asn His Ile Ile Lys Asp Gln Leu Ala Ser Lys Tyr Leu Tyr His Gly						
	370		375		380	
Gln Thr Leu Glu Thr Leu Gly Gly Lys Lys Leu Arg Val Phe Val Tyr						
385		390		395		400
Arg Asn Ser Leu Cys Ile Glu Asn Ser Cys Ile Ala Ala His Asp Lys						
	405		410		415	
Arg Gly Arg Tyr Gly Thr Leu Phe Thr Met Asp Arg Val Leu Thr Pro						
	420		425		430	
Pro Met Gly Thr Val Met Asp Val Leu Lys Gly Asp Asn Arg Phe Ser						
	435		440		445	
Met Leu Val Ala Ala Ile Gln Ser Ala Gly Leu Thr Glu Thr Leu Asn						

450	455	460
Arg Glu Gly Val Tyr Thr Val Phe Ala Pro Thr Asn Glu Ala Phe Arg		
465	470	475 480
Ala Leu Pro Pro Arg Glu Arg Ser Arg Leu Leu Gly Asp Ala Lys Glu		
485	490	495
Leu Ala Asn Ile Leu Lys Tyr His Ile Gly Asp Glu Ile Leu Val Ser		
500	505	510
Gly Gly Ile Gly Ala Leu Val Arg Leu Lys Ser Leu Gln Gly Asp Lys		
515	520	525
Leu Glu Val Ser Leu Lys Asn Asn Val Val Ser Val Asn Lys Glu Pro		
530	535	540
Val Ala Glu Pro Asp Ile Met Ala Thr Asn Gly Val Val His Val Ile		
545	550	555 560
Thr Asn Val Leu Gln Pro Pro Ala Asn Arg Pro Gln Glu Arg Gly Asp		
565	570	575
Glu Leu Ala Asp Ser Ala Leu Glu Ile		
580	585	

<210> 4
 <211> 1857
 <212> DNA
 <213> Mouse Intracisternal A-particle

<400> 4	
gcagggtcccg ccaagtcacc ctaccagctg gtgctgcagc atagccgget ccggggtcgc	60
cagcacggcc ccaatgtatg tgctgtgcag aaggtcattg gcaccaacaa gaaatacttc	120
accaactgca agcagtggta ccagaggaag atctgcgga agtcgacagt catcagttat	180
gagtgtgtgc ctggatatga aaagggtcca ggagagaaag gttgcccagc agctcttccg	240
ctctcaaadc tgtatgagac catgggagtt gtgggatcga ccaccacaca gctgtataca	300
gaccgcacag aaaagctgag gcctgagatg gagggaccgc gaagcttcac catctttgct	360
cctagcaatg aggctgtgtc ttccttgccct gcggaagtgc tggactccct ggtgagcaac	420
gtcaacatcg aactgctcaa tgctctccgc taccacatgg tggacaggcg ggtcctgacc	480
gatgagctca agcacggcat gaccctcacc tccatgtacc agaattccaa catccagatc	540
catcactatc ccaatgggat tgtaactgtt aactgtgccc ggctgtgaa ggctgaccac	600
catgcgacca acggcggtgt gcactctatt gacaagggtca tttccaccat caccaacaac	660
atccagcaga tcattgaaat cgaggacacc tttgagacac ttcgggccgc cgtggctgca	720

tcaggactca ataccgtgct ggagggcgac ggccagttca cactcttggc cccaaccaac	780
gaggcctttg agaagatccc tgccgagacc ttgaaccgca tcctgggtga ccagaggca	840
ctgagagacc tgctaaacaa ccacatcctg aagtcagcca tgtgtgctga ggccattgta	900
gctggaatgt ccatggagac cctggggggc accacactgg aggtgggctg cagtggggac	960
aagctcacca tcaacgggaa ggctgtcatc tccaacaaag acatcctggc caccaacggt	1020
gtcattcatt tcattgatga gctgcttata ccagattcag ccaagacact gcttgagctg	1080
gctggggaat ctgacgtctc cactgccatt gacatcctca aacaagctgg cctcgatact	1140
catctctctg ggaaagaaca gttgaccttc ctggccccc tgaattctgt gttcaaagat	1200
ggtgtccctc gcatcgacgc ccagatgaag actttgcttc tgaaccacat ggtcaaagaa	1260
cagttggcct ccaagtatct gtactctgga cagacactgg acacgctggg tggcaaaaag	1320
ctgcgagtct ttgtttatcg aaatagcctc tgcattgaaa acagctgcat tgctgcccat	1380
gataagaggg gacggtttgg gaccctgttc accatggacc ggatgttgac accccaatg	1440
gggacagtta tggatgtcct gaagggagac aatcgtttta gcatgctggt ggccgccatc	1500
cagtctgcag gactcatgga gatcctcaac cggaagggg tctacactgt ttttgcctcc	1560
accaatgaag cgttccaagc catgcctcca gaagaactga acaaactctt ggcaaatgcc	1620
aaggaaactta ccaacatcct gaagtaccac attggtgatg aaatcctggt tagcggaggc	1680
atcggggccc tgggtgaggct gaagtctctc caaggggaca aactggaagt cagctcgaaa	1740
aacaatgtag tgagtgtcaa taaggagcct gttgccgaaa ccgacatcat ggccacaaac	1800
ggtgtggtct atgcatcaa cactgttctg cagccgccag ccaaccgacc acaagaa	1857

<210> 5
 <211> 609
 <212> PRT
 <213> Mouse Intracisternal A-particle

 <220>
 <221> PEPTIDE
 <222> (1)..(609)
 <223> 23 to 641 amino acid sequence of mouse

<400> 5
 Ala Gly Pro Ala Lys Ser Pro Tyr Gln Leu Val Leu Gln His Ser Arg
 1 5 10 15
 Leu Arg Gly Arg Gln His Gly Pro Asn Val Cys Ala Val Gln Lys Val
 20 25 30

Ile	Gly	Thr	Asn	Arg	Lys	Tyr	Phe	Thr	Asn	Cys	Lys	Gln	Trp	Tyr	Gln	35	40	45	
Arg	Lys	Ile	Cys	Gly	Lys	Ser	Thr	Val	Ile	Ser	Tyr	Glu	Cys	Cys	Pro	50	55	60	
Gly	Tyr	Glu	Lys	Val	Pro	Gly	Glu	Lys	Gly	Cys	Pro	Ala	Ala	Leu	Pro	65	70	75	80
Leu	Ser	Asn	Leu	Tyr	Glu	Thr	Leu	Gly	Val	Val	Gly	Ser	Thr	Thr	Thr	85	90	95	
Gln	Leu	Tyr	Thr	Asp	Arg	Thr	Glu	Lys	Leu	Arg	Pro	Glu	Met	Glu	Gly	100	105	110	
Pro	Gly	Ser	Phe	Thr	Ile	Phe	Ala	Pro	Ser	Asn	Glu	Ala	Trp	Ala	Ser	115	120	125	
Leu	Pro	Ala	Glu	Val	Leu	Asp	Ser	Leu	Val	Ser	Asn	Val	Asn	Ile	Glu	130	135	140	
Leu	Leu	Asn	Ala	Leu	Arg	Tyr	His	Met	Val	Gly	Arg	Arg	Val	Leu	Thr	145	150	155	160
Asp	Glu	Leu	Lys	His	Gly	Met	Thr	Leu	Thr	Ser	Met	Tyr	Gln	Asn	Ser	165	170	175	
Asn	Ile	Gln	Ile	His	His	Tyr	Pro	Asn	Gly	Ile	Val	Thr	Val	Asn	Cys	180	185	190	
Ala	Arg	Leu	Leu	Lys	Ala	Asp	His	His	Ala	Thr	Asn	Gly	Val	Val	His	195	200	205	
Leu	Ile	Asp	Lys	Val	Ile	Ser	Thr	Ile	Thr	Asn	Asn	Ile	Gln	Gln	Ile	210	215	220	
Ile	Glu	Ile	Glu	Asp	Thr	Phe	Glu	Thr	Leu	Arg	Ala	Ala	Va						